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<110> Jacquemin, Marc
Saint-Remy, Jean-Marie

<120> Variable antibodies

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<140> US 10/566,851
<141> 2006-02-01

<150> PCT/BE04/000118
<151> 2004-08-16

<150> GB 0319118.6
<151> 2003-08-14

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<151> 2003-08-18

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<170> PatentIn version 3.5

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tgcaagacct ctggatacaa cttcaccggc tactctgctt ctggacatat cttcaccgcc 180

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aaccctaaca gtggtgccac agactatgca cataaatttc agggcagggt caccatgtcc 300

agggacacgt ccatcagcac agcctacatg gaactgagca ggctgacatc tgacgacacg 360

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Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
35 40 45

Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
50 55 60

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
65 70 75 80

Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg

85 90 95

Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
100 105 110

Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala
115 120 125

Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp
130 135 140

Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
145 150 155 160

Gly Pro Ser Val Phe
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ctctcctgca gggccagtca gagtgttgcc agcgcctact tagcctggta ccagcaaaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca gtagggccac cgacatccca 240

cacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300

cctgaagatt ttgcagtgta ctactgtcag caatatggta cctcagcctt actcactttc 360

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
65 70 75 80

His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr

100 105 110

Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
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cccaagcttc caccatggaa accccagckc agct 34

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<212> DNA
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<400> 10
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<223> Krix-1 forward mutagenic primer Asn47Glu

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<400> 19
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<212> DNA
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<210> 21
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<212> DNA
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ctctcctgca gggccagtca gagtgttgcc agcgcctact tagcctggta ccagcaaaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca gtagggccac cgacatccca 240

cacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300

cctgaagatt ttgcagtgta ctactgtcag caatatggta cctcagcctt actcactttc 360

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gcctcagtga aggtctcctg caagacctct ggataccaat tcaccggcta ctctgcttct 540

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
65 70 75 80

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His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110

Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
        115                 120                 125

Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
145                 150                 155                 160

Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly
                165                 170                 175

Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val
            180                 185                 190

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro
        195                 200                 205

Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr
    210                 215                 220

Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg
225                 230                 235                 240

Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala Asp Asn
                245                 250                 255

Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp Tyr Trp
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Gly Arg Gly Thr Leu Val Thr Val Ser Ser His His His His His His
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<210> 28
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<212> DNA
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<220>
<223> CHO-scFvKRIX-1VLVHQ(His) reverse primer

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tgcaaggctt ctggaggcac cttcagcagc tttggtatca gctgggtgcg acaggcccct 180

ggacaagggc ttgagtgggt gggagggatc atccctatct ttggtacagc aaacaccgca 240

cggaacttcc agaatagagt caccattacc gcggacgaat tcacgagcac agcctacata 300

cgactgagga gcctgagatc tgaagatacg gccgtgtatt actgtgtcgg cggtcgagat 360

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Pro Gly Ser Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
        35                  40                  45

Ser Ser Phe Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Val Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Thr Ala
65                  70                  75                  80

Arg Asn Phe Gln Asn Arg Val Thr Ile Thr Ala Asp Glu Phe Thr Ser
                85                  90                  95

Thr Ala Tyr Ile Arg Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Val Gly Gly Arg Asp Ala Tyr Ser Phe Asp Gly Phe Asp
        115                 120                 125

Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
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Gly Pro Ser Val Phe Pro
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tgctctagag ataagttggg tcataaattt gcttcctggt atcaacagaa gccaggccag 180

tcccctgctc ttctcatcta tcaagacagc aagcggccct cagggatccc tgagcgattc 240

tctggctcca actctgggaa cacagccact ctgaccatca gcgggaccca ggctatggat 300

gaggctgact attactgtca ggcgtgggac aacaccactg ccgtattcgg cggagggacc 360

aagttgacag tcctaagtca gcccaaggct gccccctcgg tcactctgtt cccgccctcc 420

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<223> CDR2

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<223> CDR3

<400> 32

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Ser Val Ala Ser Ser Gly Leu Thr Gln Pro His Ser Val Ser Val Ser
            20                  25                  30

Pro Gly Gln Thr Ala Asn Ile Thr Cys Ser Arg Asp Lys Leu Gly His
        35                  40                  45

Lys Phe Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Ala Leu
    50                  55                  60

Leu Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
65                  70                  75                  80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
                85                  90                  95

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Asn Thr
            100                 105                 110

Thr Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
        115                 120                 125

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
    130                 135                 140
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Tyr Ser Val His
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<400> 34

Arg Ile Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln
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Gly

<210> 35
<211> 18
<212> PRT
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<220>
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<400> 35

Ala Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe
1 5 10 15

Asp Tyr

<210> 36
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Arg Ala Ser Gln Ser Val Ala Ser Ala Tyr Leu Ala

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